

#### FIGURE 1a

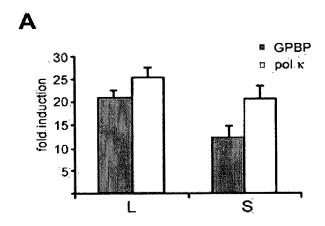
9	180	270	360	450
ON-GPBP-18m   GGCATGGTTAACGTGGTTATGTTTTATTTACAACCAAGAAAATCCCAGGCTATCATCTCACATTCTTGTTTTACTTTAAA   CCGTACCAATTGCACCAAGAGTCATTCTATAAGTAAATGTTGGTTCTTTTAGGGTCCGATAGTAGAGTGTAAGAACAAATGAAATTTT	Xbal AACCTTTCTAACGTCATTTATTCTCTGACAACCTCAAAATTACTTTCTACAAAGCAAACTCTAAGAAATCTAAAAATGCGAAGTGCGTGC	TGTGAGAAGGTACTAAGGAAATTCTTCCTTTAAACGTCAAATGTGAATTCTAACTTCTAATGAGTAAGACCCTCGAGATTTACAGCGGTG ACACTCTTCCATGATTCCTTTAAGAAGGAAATTTGCAGTTTACACTTAAGATTGAAGATTACTCATTCTGGGAGCTCTAAATGTCGCCAC	GICTGGTGGAAAGAAAACCCTTGGCACTAGTAGCTCACAAAACCCCAGCCCATGGTTGAGGGGGAAGCGGCCAGATGCTCCCGGGCTTTG CAGACCACCTTTCTTTGGGAACCGTGATCATCGAGTGTTTTGGGGTCGGGTACCAACTCCGCCTTCGCCGGTCTACGAGGGCCCGAAAA	Apal  GACAAGCCGCCCTGGAAAGCAGGCCCGTCATCTTCAGCGGAAAGCTCTCTCACGTCTGGGGCCCGGGAGGGTTCGTCGTCATAACA  CTGTTCGGCGGGACCTTTCGTCCGGGCAGTAGAAGTCGCCTTTCGAGAAGTGCAGACCGGGGCGTTCGGGGCCTCCCAAGCAGTATTTGT  HeLa 4.1 ← → → → → → → → → → → → → → → → → → →

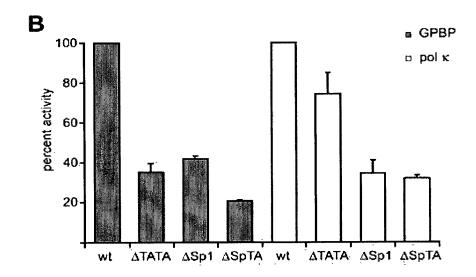


### FIGURE 1b

630	720	810	006	, 0 50 50
AAGCGATCCCCGCGGGATACTCACCGTTACCTCAGGATCGCGACTACAACTCCCAGGAGGCTGCGGAGGCGAGGCGAACGAA	Sp1  CCCAGAATGCAGCACACACCTGCATCCCTACCCCTCTCTTTTTCTCCGCTCCTTTTTTTT	Sp1 Sp1 AGGTTCGGGAGGATCCCGAAGGCTCGGCGTGTCGCGTCAGACGCGGGGGGGG	Fan 1 COL4A3BP  GGAGGAAGGGGAAAGGGGAAGGGGAGGGAGGGTAATAQTGGGCAGGCAGGAAGATGGCGGCGGTAGCGGAGGTGTGAGTG  GCAGGACGAAGGGGAAAGGACAGGGGAAGGGGAGGGA	ECIXI GACGCGGGACTCAGCGGATTTTCTCTTCCCTTTTTCCCTTTCCC CTGCGCCCTGAGTCGCCTAAAAGGAAAAAAAAAA





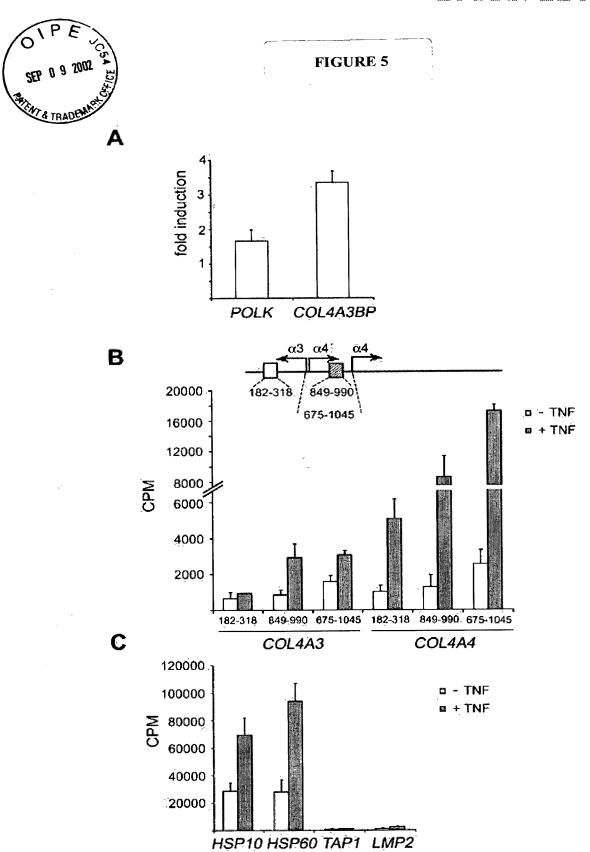




COL4A3BP
Region aligned 469-608 $Q=620; E(Q)=591.4\pm17.1$ $=1.6725 P=0.00472$
Region aligned 849-990 Q=674; E(Q)=568.7±17.5 z=6.0171, <b>P&lt;0.0001</b>
Region aligned 1714-1853 <i>Q</i> =570; <i>E</i> ( <i>Q</i> )=524.2±18.4 <i>z</i> =2.4891, <i>P</i> = <b>0.0064</b>



Alignment map*	LMP2 TAP!	DHFR DHFR'  MRPI		HRS HRS'	HSP10 HSP60	
POLK	Region aligned 27355-27494 $Q$ =620; $E(Q)$ =582.8±18.6 $z$ =2, $P$ =0.0228	Region aligned 704-843 $Q$ =640; $E(Q)$ =553.4±18.1 $z$ =4.7845, <b>P&lt;0.0001</b>	Region aligned 561-705 $Q=565$ ; $E(Q)=549.4\pm18.4$ $z=0.8478$ , $P=0.1983$	Region aligned 214-353 $Q=560$ ; $E(Q)=557.1\pm16.2$ $z=0.1790$ , $P=0.4290$	Region aligned 3684-3821 Q=594; E(Q)=542.6±17.1 z=3.0058, <b>P=0.0013</b>	Region aligned 14190-14329 $Q$ =610; $E(Q)$ =601.9±15.5 $z$ =0.5226, $P$ =0.3006
COL4A3BP ₪	Region aligned 24579-24718 $Q$ =610; $E(Q)$ =549.9±16.9 $z$ =3.5562, $P$ =0.0002	Region aligned 849-991 $Q=581$ ; $E(Q)=557.7\pm20.8$ $z=1.1202$ , $P=0.1313$	Region aligned 632-769 $Q=554$ ; $E(Q)=573.4\pm20.4$ $z=-0.9510$ , $P=0.8292$	Region aligned 313-452 $Q=600$ ; $E(Q)=531\pm17.5$ $z=3.9429$ , $P<0.0001$	Region aligned 3451-3590 $Q=600$ ; $E(Q)=546.7\pm16.7$ $z=3.1916$ , $P=0.0007$	Region aligned 16283-16422 Q=622; E(Q)=594.8±16.5 z=2.7394, P=0.0031
	LMP2-TAP1 GenBank no. X66401	MRP1-DHFR GenBank no. K01612	GPAT-AIRC GenBank no. U00239	<i>HO3-HRS</i> GenBank no. M96646	HSP10-HSP60 GenBank no. AJ250915	IDHG-TRAPD GenBank no. Z68129





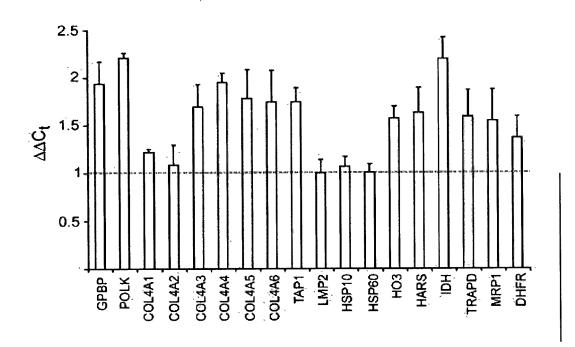
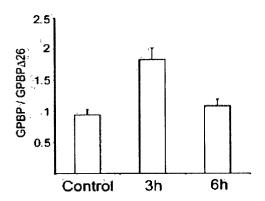
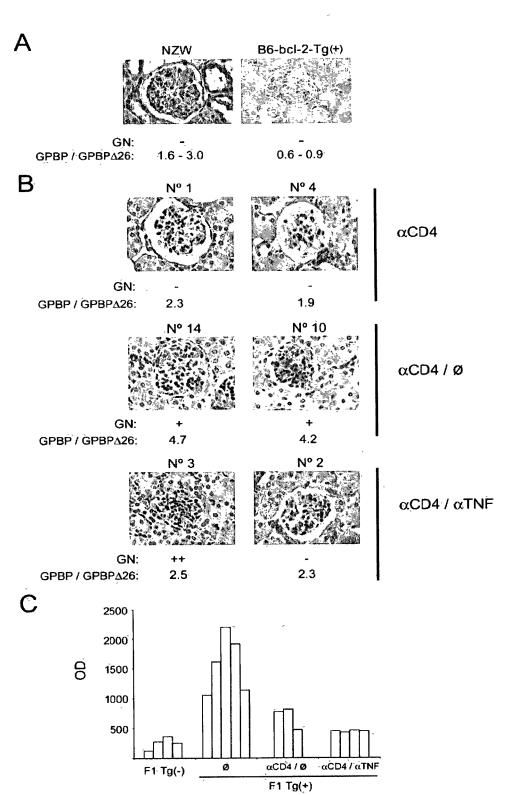




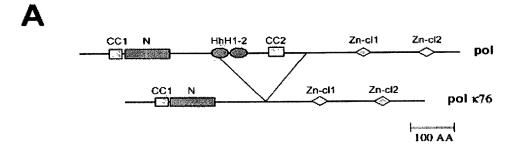
FIGURE 7

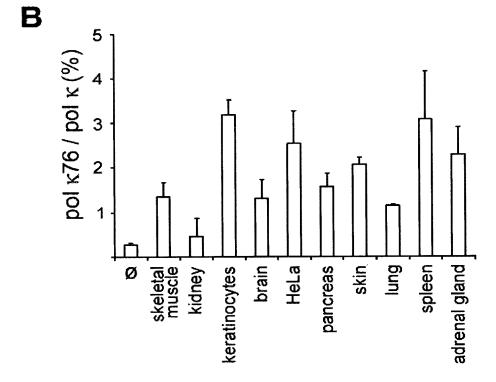




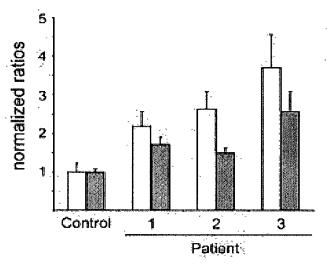












- D. GPBP / GPBPA26
- pok k767 pol w